



-1-

SEQUENCE LISTING

<110> Umana, Pablo
Bruenker, Peter
Ferrara, Claudia
Suter, Tobias

<120> Fusion Constructs and Use of Same to Produce Antibodies with
Increased Fc Receptor Binding Affinity and Effector Function

<130> 1975.0180003

<140> US 10/761,435
<141> 2004-01/22

<150> US 60/441,307
<151> 2003-01-22

<150> US 60/491,254
<151> 2003-07-31

<150> US 60/495,142
<151> 2003-08-15

<160> 20

<170> PatentIn version 3.2

<210> 1
<211> 11
<212> PRT
<213> Unknown

<220>
<223> c-myc epitope tag

<400> 1

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-177 PCR primer

<400> 2
gcgtgtgcct gtgacccccg cgcccctgct ccagccactg tcccc 45

<210> 3
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-178 PCR primer

<400> 3
gaaggtttct ccagcatcct ggtacc 26

<210> 4
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-179 PCR primer

<400> 4
ctgaggcgcg ccgccaccat gctgaagaag cagtctgcag ggc 43

<210> 5
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-180 PCR primer

<400> 5
ggggacagtg gctggagcag gggcgcgggg gtcacaggca cacgcggc 48

<210> 6
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-252 PCR primer

<400> 6
gctaggccgg ccgccaccat gaagttaagc cgccagttca ccgtgttcgg 50

<210> 7
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-253 PCR primer

<400> 7
ggggacagtg gctggagcag gggtagacca gcaccttggc tgaaattgct ttgtgaactt 60
ttcgg 65

<210> 8
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-254 PCR primer

<400> 8
tccgaaaagt tcacaaagca atttcagcca aggtgctggc tcacccctgc tccagccact 60
gtcccc 66

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-255 PCR primer

<400> 9
atgccgcata ggctccgag caggacccc 29

<210> 10
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-261 PCR primer

<400> 10
gctaaatatt gaattccctt tatgtgtaac tcttggtga agc 43

<210> 11
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-262 PCR primer

<400> 11
tagcaatatt gaattcgag gaaaaggaca agcagcgaaa attcacgc 48

<210> 12
<211> 1715
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of GnTI-GnTIII

<400> 12
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
tcgctctacc tgatgctgga ccgggggtcac ttagactacc ccaggaaccc gcgccgcgag 120
ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180
ttgctagctg agaataatga gatcatctca aatattagag actcagtcac caatttgagt 240
gagtctgtgg aggatgggtcc gaaaagttca caaagcaatt tcagccaagg tgctgggtca 300
ccctgctcc agccactgtc ccctagcaag gccaccgaag aactgcaccg ggtggacttc 360

```

gtgttgccgg aggacaccac agagtatttt gtgcgcacca aagctggcgg tgtgtgcttc 420
aaaccaggta ccaggatgct ggagaaacct tctccagggc ggacagagga gaagaccaag 480
gtggctgagg ggtcctcggg ccgggggcct gctcggaggc ctatgcggca tgtgttgagt 540
gcacgggagc gcctgggagg ccggggcact aggcgcaagt gggttgagtg tgtgtgcctg 600
ccaggctggc acgggcccag ctgcgggggtg cccactgtgg tccagtattc caacctgccc 660
accaaggagc gcctggtacc caggagggtg ccgaggcggg ttatcaacgc catcaacatc 720
aaccatgagt tcgacctgct ggatgtgcgc ttccatgagc tgggcgatgt tgtggacgcc 780
tttgtggtct gcgaatccaa tttcaccgcc tacggggagc ctcgccgct caagttccga 840
gagatgctga ccaatggcac cttcgagtac atccgccaca aggtgctcta cgtcttctg 900
gaccacttcc cacctggtgg ccgtcaggac ggctggattg cagacgacta cctgcgtacc 960
ttcctcacc aggatggtgt ctccgcctg cgcaacctgc gacctgatga cgtctttatc 1020
atcgacgacg cggacgagat ccctgcgcgt gatggtgtgc tgttcctcaa gctctacgat 1080
ggctggacag agcccttcgc cttccatag cgcaagtccc tgtatggttt cttttggaag 1140
caaccaggca cacggagggtg gtgtcaggct gcaccattga catgctgcag gctgtgtatg 1200
ggctggacgg catccgcctg cgccgccgtc agtactacac catgcccac tttcgacagt 1260
atgagaaccg caccggccac atcctagtgc agtggtctct cggcagcccc ctgcacttcg 1320
cgggctggca ctgctcctgg tgcttcacac ccgagggcat ctacttcaaa ctcggtgcgg 1380
cccagaatgg tgacttcccc cgctgggggtg actacgagga caagagggac ctcaattaca 1440
tccgaagctt gattcgcact gggggatggt tcgacggcac gcagcaggag taccctctg 1500
cagaccccag tgaacacatg tatgctccta agtacctgct caagaactat gaccagttcc 1560
gctacttgct cgaaaatccc taccgggagc ccaagagcac tgtagagggt gggcgccgga 1620
accagggtc agacggaagg tcactgtctg tcaggggcaa gttggataca acggagggcc 1680
cggaacagaa actgatctct gaagaggacc tgtag 1715

```

<210> 13

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of GnTI-GnTIII

<400> 13

```

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1           5           10          15

```

```

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp

```

20					25					30					
Tyr	Pro	Arg	Asn	Pro	Arg	Arg	Glu	Gly	Ser	Phe	Pro	Gln	Gly	Gln	Leu
	35						40					45			
Ser	Met	Leu	Gln	Glu	Lys	Ile	Asp	His	Leu	Glu	Arg	Leu	Leu	Ala	Glu
	50					55					60				
Asn	Asn	Glu	Ile	Ile	Ser	Asn	Ile	Arg	Asp	Ser	Val	Ile	Asn	Leu	Ser
65					70					75					80
Glu	Ser	Val	Glu	Asp	Gly	Pro	Lys	Ser	Ser	Gln	Ser	Asn	Phe	Ser	Gln
				85					90					95	
Gly	Ala	Gly	Ser	Pro	Leu	Leu	Gln	Pro	Leu	Ser	Pro	Ser	Lys	Ala	Thr
			100					105					110		
Glu	Glu	Leu	His	Arg	Val	Asp	Phe	Val	Leu	Pro	Glu	Asp	Thr	Thr	Glu
		115					120					125			
Tyr	Phe	Val	Arg	Thr	Lys	Ala	Gly	Gly	Val	Cys	Phe	Lys	Pro	Gly	Thr
	130					135					140				
Arg	Met	Leu	Glu	Lys	Pro	Ser	Pro	Gly	Arg	Thr	Glu	Glu	Lys	Thr	Lys
145					150					155					160
Val	Ala	Glu	Gly	Ser	Ser	Val	Arg	Gly	Pro	Ala	Arg	Arg	Pro	Met	Arg
				165					170					175	
His	Val	Leu	Ser	Ala	Arg	Glu	Arg	Leu	Gly	Gly	Arg	Gly	Thr	Arg	Arg
			180					185					190		
Lys	Trp	Val	Glu	Cys	Val	Cys	Leu	Pro	Gly	Trp	His	Gly	Pro	Ser	Cys
		195					200					205			
Gly	Val	Pro	Thr	Val	Val	Gln	Tyr	Ser	Asn	Leu	Pro	Thr	Lys	Glu	Arg
	210					215					220				
Leu	Val	Pro	Arg	Glu	Val	Pro	Arg	Arg	Val	Ile	Asn	Ala	Ile	Asn	Ile
225					230					235					240
Asn	His	Glu	Phe	Asp	Leu	Leu	Asp	Val	Arg	Phe	His	Glu	Leu	Gly	Asp
				245					250					255	
Val	Val	Asp	Ala	Phe	Val	Val	Cys	Glu	Ser	Asn	Phe	Thr	Ala	Tyr	Gly
			260					265					270		

Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly Thr Phe
275 280 285

Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His Phe Pro
290 295 300

Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu Arg Thr
305 310 315 320

Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg Pro Asp
325 330 335

Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg Asp Gly
340 345 350

Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe Ala Phe
355 360 365

His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro Gly Thr
370 375 380

Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala Val Tyr
385 390 395 400

Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr Met Pro
405 410 415

Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val Gln Trp
420 425 430

Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser Trp Cys
435 440 445

Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln Asn Gly
450 455 460

Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu Asn Tyr
465 470 475 480

Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr Gln Gln
485 490 495

Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro Lys Tyr
500 505 510

Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn Pro Tyr
515 520 525

Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln Gly Ser
530 535 540

Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr Glu Gly
545 550 555 560

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
565 570

<210> 14
<211> 1722
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GnTIII

<400> 14
atgctgaaga agcagtctgc agggcttgtg ctgtggggcg ctatcctctt tgtggcctgg 60
aatgccctgc tgctcctctt cttctggacg cgcccagcac ctggcaggcc accctcagtc 120
agcgctctcg atggcgaccc cgccagcctc acccggaag tgattcgctt ggcccaagac 180
gccgaggtgg agctggagcg gcagcgtggg ctgctgcagc agatcgggga tgccctgtcg 240
agccagcggg ggaggggtgcc caccgcggcc cctcccgcc agccgcgtgt gcctgtgacc 300
cccgcgcccc tgctccagcc actgtcccct agcaaggcca ccgaagaact gcaccgggtg 360
gacttcgtgt tgccggagga caccacagag tattttgtgc gcaccaaagc tggcgggtgtg 420
tgcttcaaac caggtaccag gatgctggag aaaccttctc cagggcggac agaggagaag 480
accaaggtgg ctgaggggtc ctcggtccgg ggtcctgctc ggaggcctat gcggcatgtg 540
ttgagtgcac gggagcgcct gggaggccgg ggcactaggc gcaagtgggt tgagtgtgtg 600
tgctgccag gctggcacgg gccagctgc ggggtgcca ctgtggtcca gtattccaac 660
ctgcccacca aggagcgcct ggtaccagg gaggtgccga ggcgggttat caacgccatc 720
aacatcaacc atgagttcga cctgctggat gtgcgttcc atgagctggg cgatgttgtg 780
gacgcctttg tggctctgca atccaatttc accgcctacg gggagcctcg gccgctcaag 840
ttccgagaga tgctgaccaa tggcaccttc gagtacatcc gccacaaggt gctctacgtc 900
ttcctggacc acttcccacc tgggtggcgt caggacggct ggattgcaga cgactacctg 960
cgtaccttcc tcaaccagga tgggtgtctc cgctgcgca acctgcgacc tgatgacgtc 1020
tttatcatcg acgacgcgga cgagatccct gcgcgtgatg gtgtgctgtt cctcaagctc 1080
tacgatggct ggacagagcc cttcgccttc catatgcgca agtccttgta tggtttcttt 1140
tggaagcaac caggcacact ggaggtgggtg tcaggctgca ccattgacat gctgcaggct 1200

gtgtatgggc tggacggcat ccgcctgcgc cgccgtcagt actacaccat gcccaacttt 1260
cgacagtatg agaaccgcac cggccacatc ctagtgacgt ggtctctcgg cagccccctg 1320
cacttcgcgg gctggcactg ctcctggtgc ttcacacccg agggcatcta cttcaaactc 1380
gtgtcggccc agaatggtga cttccccgcg tggggtgact acgaggacaa gagggacctc 1440
aattacatcc gaagcttgat tcgcactggg ggatggttcg acggcacgca gcaggagtac 1500
cctcctgcag accccagtga acacatgtat gctcctaagt acctgctcaa gaactatgac 1560
cagttccgct acttgctcga aaatccctac cgggagccca agagcactgt agaggggtggg 1620
cgccggaacc agggctcaga cggaaggcca tctgctgtca ggggcaagtt ggatacaacg 1680
gagggcccgg aacagaaact gatctctgaa gaggacctgt ag 1722

<210> 15

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of ManII-GnTIII fusion

<400> 15

Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
1 5 10 15

Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro
20 25 30

Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser
65 70 75 80

Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg
85 90 95

Val Pro Val Thr Pro Ala Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys
100 105 110

Ala Thr Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr
115 120 125

Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro

130					135					140					
Gly	Thr	Arg	Met	Leu	Glu	Lys	Pro	Ser	Pro	Gly	Arg	Thr	Glu	Glu	Lys
145					150					155					160
Thr	Lys	Val	Ala	Glu	Gly	Ser	Ser	Val	Arg	Gly	Pro	Ala	Arg	Arg	Pro
				165					170					175	
Met	Arg	His	Val	Leu	Ser	Ala	Arg	Glu	Arg	Leu	Gly	Gly	Arg	Gly	Thr
			180					185					190		
Arg	Arg	Lys	Trp	Val	Glu	Cys	Val	Cys	Leu	Pro	Gly	Trp	His	Gly	Pro
		195					200					205			
Ser	Cys	Gly	Val	Pro	Thr	Val	Val	Gln	Tyr	Ser	Asn	Leu	Pro	Thr	Lys
	210					215					220				
Glu	Arg	Leu	Val	Pro	Arg	Glu	Val	Pro	Arg	Arg	Val	Ile	Asn	Ala	Ile
225					230					235					240
Asn	Ile	Asn	His	Glu	Phe	Asp	Leu	Leu	Asp	Val	Arg	Phe	His	Glu	Leu
				245					250					255	
Gly	Asp	Val	Val	Asp	Ala	Phe	Val	Val	Cys	Glu	Ser	Asn	Phe	Thr	Ala
			260					265					270		
Tyr	Gly	Glu	Pro	Arg	Pro	Leu	Lys	Phe	Arg	Glu	Met	Leu	Thr	Asn	Gly
	275						280					285			
Thr	Phe	Glu	Tyr	Ile	Arg	His	Lys	Val	Leu	Tyr	Val	Phe	Leu	Asp	His
	290					295					300				
Phe	Pro	Pro	Gly	Gly	Arg	Gln	Asp	Gly	Trp	Ile	Ala	Asp	Asp	Tyr	Leu
305					310					315					320
Arg	Thr	Phe	Leu	Thr	Gln	Asp	Gly	Val	Ser	Arg	Leu	Arg	Asn	Leu	Arg
				325					330					335	
Pro	Asp	Asp	Val	Phe	Ile	Ile	Asp	Asp	Ala	Asp	Glu	Ile	Pro	Ala	Arg
			340					345					350		
Asp	Gly	Val	Leu	Phe	Leu	Lys	Leu	Tyr	Asp	Gly	Trp	Thr	Glu	Pro	Phe
		355					360					365			
Ala	Phe	His	Met	Arg	Lys	Ser	Leu	Tyr	Gly	Phe	Phe	Trp	Lys	Gln	Pro
	370					375					380				

Gly Thr Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala
385 390 395 400

Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr
405 410 415

Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val
420 425 430

Gln Trp Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser
435 440 445

Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln
450 455 460

Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu
465 470 475 480

Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr
485 490 495

Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro
500 505 510

Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn
515 520 525

Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln
530 535 540

Gly Ser Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr
545 550 555 560

Glu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
565 570

<210> 16
<211> 398
<212> PRT
<213> Unknown

<220>
<223> GalT amino acid sequence from pBlueGalT

<400> 16

Met Arg Leu Arg Glu Pro Leu Leu Ser Gly Ser Ala Ala Met Pro Gly
1 5 10 15

Ala	Ser	Leu	Gln	Arg	Ala	Cys	Arg	Leu	Leu	Val	Ala	Val	Cys	Ala	Leu	20	25	30	
His	Leu	Gly	Val	Thr	Leu	Val	Tyr	Tyr	Leu	Ala	Gly	Arg	Asp	Leu	Ser	35	40	45	
Arg	Leu	Pro	Gln	Leu	Val	Gly	Val	Ser	Thr	Pro	Leu	Gln	Gly	Gly	Ser	50	55	60	
Asn	Ser	Ala	Ala	Ala	Ile	Gly	Gln	Ser	Ser	Gly	Glu	Leu	Arg	Thr	Gly	65	70	75	80
Gly	Ala	Arg	Pro	Pro	Pro	Pro	Leu	Gly	Ala	Ser	Ser	Gln	Pro	Arg	Pro	85	90	95	
Gly	Gly	Asp	Ser	Ser	Pro	Val	Val	Asp	Ser	Gly	Pro	Gly	Pro	Ala	Ser	100	105	110	
Asn	Leu	Thr	Ser	Val	Pro	Val	Pro	His	Thr	Thr	Ala	Leu	Ser	Leu	Pro	115	120	125	
Ala	Cys	Pro	Glu	Glu	Ser	Pro	Leu	Leu	Val	Gly	Pro	Met	Leu	Ile	Glu	130	135	140	
Phe	Asn	Met	Pro	Val	Asp	Leu	Glu	Leu	Val	Ala	Lys	Gln	Asn	Pro	Asn	145	150	155	160
Val	Lys	Met	Gly	Gly	Arg	Tyr	Ala	Pro	Arg	Asp	Cys	Val	Ser	Pro	His	165	170	175	
Lys	Val	Ala	Ile	Ile	Ile	Pro	Phe	Arg	Asn	Arg	Gln	Glu	His	Leu	Lys	180	185	190	
Tyr	Trp	Leu	Tyr	Tyr	Leu	His	Pro	Val	Leu	Gln	Arg	Gln	Gln	Leu	Asp	195	200	205	
Tyr	Gly	Ile	Tyr	Val	Ile	Asn	Gln	Ala	Gly	Asp	Thr	Ile	Phe	Asn	Arg	210	215	220	
Ala	Lys	Leu	Leu	Asn	Val	Gly	Phe	Gln	Glu	Ala	Leu	Lys	Asp	Tyr	Asp	225	230	235	240
Tyr	Thr	Cys	Phe	Val	Phe	Ser	Asp	Val	Asp	Leu	Ile	Pro	Met	Asn	Asp	245	250	255	
His	Asn	Ala	Tyr	Arg	Cys	Phe	Ser	Gln	Pro	Arg	His	Ile	Ser	Val	Ala	260	265	270	

Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr Phe Gly Gly
275 280 285

Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn Gly Phe Pro
290 295 300

Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile Phe Asn Arg
305 310 315 320

Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala Val Val Gly
325 330 335

Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn Glu Pro Asn
340 345 350

Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr Met Leu Ser
355 360 365

Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val Gln Arg Tyr
370 375 380

Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro Ser
385 390 395

<210> 17
<211> 3435
<212> DNA
<213> Homo sapiens

<400> 17
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
tcgctctacc tgatgctgga ccgggggtcac ttagactacc ccaggaaccc gcgccgcgag 120
ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180
ttgctagctg agaataatga gatcatctca aatattagag actcagtcac caatttgagt 240
gagtctgtgg aggatgggtcc gaaaagtcca caaagcaatt tcagccaagg tgctgggtca 300
catcttctgc cctcacaatt atccctctca gttgacactg cagactgtct gtttgcttca 360
caaagtggaa gtcacaattc agatgtgcag atgttggtatg tttacagtct aatttctttt 420
gacaatccag atgggtggagt ttggaagcaa ggatttgaca ttacttatga atctaataa 480
tgggacactg aacccttca agtctttgtg gtgcctcatt ccataacga ccaggttg 540
ttgaagactt tcaatgacta ctttagagac aagactcagt atatttttaa taacatggtc 600
ctaaagctga aagaagactc acggaggaag tttatttggt ctgagatctc ttaccttca 660
aagtgggtggg atattataga tattcagaag aaggatgctg ttaaaagttt aatagaaaat 720

ggtcagcttg	aaattgtgac	aggtggctgg	gttatgcctg	atgaagctac	tccacattat	780
tttgccctaa	ttgatcaact	aattgaagga	catcagtggc	tggaaaataa	tataggagtg	840
aaacctcggg	ccggctgggc	tattgatccc	tttggacact	caccaacaat	ggcttatctt	900
ctaaaccgtg	ctggactttc	tcacatgctt	atccagagag	ttcattatgc	agttaaaaaa	960
cactttgcac	tgcataaaac	attggagttt	ttttggagac	agaattggga	tctgggatct	1020
gtcacagata	ttttatgcca	catgatgccc	ttctacagct	atgacatccc	tcacacttgt	1080
ggacctgatc	ctaaaatatg	ctgccagttt	gattttaaac	gtcttcctgg	aggcagattt	1140
ggttgtccct	ggggagtccc	cccagaaaca	atacatcctg	gaaatgtcca	aagcagggct	1200
cggatgctac	tagatcagta	ccgaaagaag	tcaaagcttt	ttcgtaccaa	agttctcctg	1260
gctccactag	gagatgattt	ccgctactgt	gaatacacgg	aatgggattt	acagtttaag	1320
aattatcagc	agctttttga	ttatatgaat	tctcagtcca	agtttaaagt	taagatacag	1380
tttggaactt	tatcagattt	ttttgatgcg	ctggataaag	cagatgaaac	tcagagagac	1440
aagggccagt	cgatgttccc	tgttttaagt	ggagattttt	tcacttatgc	cgatcgagat	1500
gatcattact	ggagtggcta	ttttacatcc	agaccctttt	acaaacgaat	ggacagaatc	1560
atggaatctc	atttaagggc	tgctgaaatt	ctttactatt	tcgccctgag	acaagctcac	1620
aaatacaaga	taaataaatt	tctctcatca	tcactttaca	cggcactgac	agaagccaga	1680
aggaatttgg	gactgtttca	acatcatgat	gctatcacag	gaactgcaaa	agactgggtg	1740
gttgtggatt	atggtaccag	actttttcat	tcgttaatgg	ttttggagaa	gataattgga	1800
aattctgcat	ttcttcttat	tttgaaggac	aaactcacat	acgactctta	ctctcctgat	1860
accttcctgg	agatggattt	gaaacaaaaa	tcacaagatt	ctctgccaca	aaaaaatata	1920
ataaggctga	gtgcggagcc	aaggtacctt	gtggtctata	atcctttaga	acaagaccga	1980
atctcgttgg	tctcagtcta	tgtgagttcc	ccgacagtgc	aagtgttctc	tgcttcagga	2040
aaacctgtgg	aagttcaagt	cagcgcagtt	tgggatacag	caaatactat	ttcagaaaca	2100
gcctatgaga	tctcttttcg	agcacatata	ccgccattgg	gactgaaagt	gtataagatt	2160
ttggaatcag	caagttcaaa	ttcacattta	gctgattatg	tcttgataaa	gaataaagta	2220
gaagatagcg	gaattttcac	cataaagaat	atgataaata	ctgaagaagg	tataacacta	2280
gagaactcct	ttgttttact	tcggtttgat	caaactggac	ttatgaagca	aatgatgact	2340
aaagaagatg	gtaaacacca	tgaagtaaat	gtgcaatttt	catggtatgg	aaccacaatt	2400
aaaagagaca	aaagtgggtc	ctacctcttc	ttacctgatg	gtaatgcaa	gccttatggt	2460
tacacaacac	cgccctttgt	cagagtgaca	catggaagga	tttattcgga	agtgacttgc	2520
ttttttgacc	atgttactca	tagagtccga	ctataaccaca	tacagggaat	agaaggacag	2580

tctgtggaag tttccaatat tgtggacatc cgaaaagtat ataaccgtga gattgcaatg 2640
aaaattttctt ctgatataaa aagccaaaat agattttata ctgacctaaa tgggtaccag 2700
attcaaccta gaatgacact gagcaaattg cctcttcaag caaatgtcta tcccatgacc 2760
acaatggcct atatccagga tgccaaacat cgtttgacac tgctctctgc tcagtcttta 2820
ggggtttcga gtttgaatag tggtcagatt gaagttatca tggatcgaag actcatgcaa 2880
gatgataatc gtggccttga gcaaggatc caggataaca agattacagc taatctatctt 2940
cgaatactac tagaaaaaag aagtgtctgtt aatacgggaag aagaaaagaa gtcggtcagt 3000
tatectttctc tccttagcca cataacttct tctctcatga atcatccagt cattccaatg 3060
gcaaataagt tcttctcacc tacccttgag ctgcaagggtg aattctctcc attacagtca 3120
tctttgcctt gtgacattca tctgggttaat ttgagaacaa tacagtcaaa ggtgggcaat 3180
gggcactcca atgaggcagc cttgatcctc cacagaaaag ggtttgattg tcggttctct 3240
agcaaaggca cagggctgtt ttgttctact actcagggaa agatattggg acagaaactt 3300
ttaaacaagt ttattgtcga aagtctcaca ccttcacac tatecttgat gcattcacct 3360
cccggcactc agaataaag tgagatcaac ttgagtcaa tggaaatcag cacattccga 3420
atccagttga ggtga 3435

<210> 18
<211> 1144
<212> PRT
<213> Homo sapiens

<400> 18
Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser His Leu Leu Pro Ser Gln Leu Ser Leu Ser Val Asp
100 105 110

Thr Ala Asp Cys Leu Phe Ala Ser Gln Ser Gly Ser His Asn Ser Asp
115 120 125

Val Gln Met Leu Asp Val Tyr Ser Leu Ile Ser Phe Asp Asn Pro Asp
130 135 140

Gly Gly Val Trp Lys Gln Gly Phe Asp Ile Thr Tyr Glu Ser Asn Glu
145 150 155 160

Trp Asp Thr Glu Pro Leu Gln Val Phe Val Val Pro His Ser His Asn
165 170 175

Asp Pro Gly Trp Leu Lys Thr Phe Asn Asp Tyr Phe Arg Asp Lys Thr
180 185 190

Gln Tyr Ile Phe Asn Asn Met Val Leu Lys Leu Lys Glu Asp Ser Arg
195 200 205

Arg Lys Phe Ile Trp Ser Glu Ile Ser Tyr Leu Ser Lys Trp Trp Asp
210 215 220

Ile Ile Asp Ile Gln Lys Lys Asp Ala Val Lys Ser Leu Ile Glu Asn
225 230 235 240

Gly Gln Leu Glu Ile Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala
245 250 255

Thr Pro His Tyr Phe Ala Leu Ile Asp Gln Leu Ile Glu Gly His Gln
260 265 270

Trp Leu Glu Asn Asn Ile Gly Val Lys Pro Arg Ser Gly Trp Ala Ile
275 280 285

Asp Pro Phe Gly His Ser Pro Thr Met Ala Tyr Leu Leu Asn Arg Ala
290 295 300

Gly Leu Ser His Met Leu Ile Gln Arg Val His Tyr Ala Val Lys Lys
305 310 315 320

His Phe Ala Leu His Lys Thr Leu Glu Phe Phe Trp Arg Gln Asn Trp
325 330 335

Asp	Leu	Gly	Ser	Val	Thr	Asp	Ile	Leu	Cys	His	Met	Met	Pro	Phe	Tyr	340	345	350	
Ser	Tyr	Asp	Ile	Pro	His	Thr	Cys	Gly	Pro	Asp	Pro	Lys	Ile	Cys	Cys	355	360	365	
Gln	Phe	Asp	Phe	Lys	Arg	Leu	Pro	Gly	Gly	Arg	Phe	Gly	Cys	Pro	Trp	370	375	380	
Gly	Val	Pro	Pro	Glu	Thr	Ile	His	Pro	Gly	Asn	Val	Gln	Ser	Arg	Ala	385	390	395	400
Arg	Met	Leu	Leu	Asp	Gln	Tyr	Arg	Lys	Lys	Ser	Lys	Leu	Phe	Arg	Thr	405	410	415	
Lys	Val	Leu	Leu	Ala	Pro	Leu	Gly	Asp	Asp	Phe	Arg	Tyr	Cys	Glu	Tyr	420	425	430	
Thr	Glu	Trp	Asp	Leu	Gln	Phe	Lys	Asn	Tyr	Gln	Gln	Leu	Phe	Asp	Tyr	435	440	445	
Met	Asn	Ser	Gln	Ser	Lys	Phe	Lys	Val	Lys	Ile	Gln	Phe	Gly	Thr	Leu	450	455	460	
Ser	Asp	Phe	Phe	Asp	Ala	Leu	Asp	Lys	Ala	Asp	Glu	Thr	Gln	Arg	Asp	465	470	475	480
Lys	Gly	Gln	Ser	Met	Phe	Pro	Val	Leu	Ser	Gly	Asp	Phe	Phe	Thr	Tyr	485	490	495	
Ala	Asp	Arg	Asp	Asp	His	Tyr	Trp	Ser	Gly	Tyr	Phe	Thr	Ser	Arg	Pro	500	505	510	
Phe	Tyr	Lys	Arg	Met	Asp	Arg	Ile	Met	Glu	Ser	His	Leu	Arg	Ala	Ala	515	520	525	
Glu	Ile	Leu	Tyr	Tyr	Phe	Ala	Leu	Arg	Gln	Ala	His	Lys	Tyr	Lys	Ile	530	535	540	
Asn	Lys	Phe	Leu	Ser	Ser	Ser	Leu	Tyr	Thr	Ala	Leu	Thr	Glu	Ala	Arg	545	550	555	560
Arg	Asn	Leu	Gly	Leu	Phe	Gln	His	His	Asp	Ala	Ile	Thr	Gly	Thr	Ala	565	570	575	
Lys	Asp	Trp	Val	Val	Val	Asp	Tyr	Gly	Thr	Arg	Leu	Phe	His	Ser	Leu	580	585	590	

Met Val Leu Glu Lys Ile Ile Gly Asn Ser Ala Phe Leu Leu Ile Leu
595 600 605

Lys Asp Lys Leu Thr Tyr Asp Ser Tyr Ser Pro Asp Thr Phe Leu Glu
610 615 620

Met Asp Leu Lys Gln Lys Ser Gln Asp Ser Leu Pro Gln Lys Asn Ile
625 630 635 640

Ile Arg Leu Ser Ala Glu Pro Arg Tyr Leu Val Val Tyr Asn Pro Leu
645 650 655

Glu Gln Asp Arg Ile Ser Leu Val Ser Val Tyr Val Ser Ser Pro Thr
660 665 670

Val Gln Val Phe Ser Ala Ser Gly Lys Pro Val Glu Val Gln Val Ser
675 680 685

Ala Val Trp Asp Thr Ala Asn Thr Ile Ser Glu Thr Ala Tyr Glu Ile
690 695 700

Ser Phe Arg Ala His Ile Pro Pro Leu Gly Leu Lys Val Tyr Lys Ile
705 710 715 720

Leu Glu Ser Ala Ser Ser Asn Ser His Leu Ala Asp Tyr Val Leu Tyr
725 730 735

Lys Asn Lys Val Glu Asp Ser Gly Ile Phe Thr Ile Lys Asn Met Ile
740 745 750

Asn Thr Glu Glu Gly Ile Thr Leu Glu Asn Ser Phe Val Leu Leu Arg
755 760 765

Phe Asp Gln Thr Gly Leu Met Lys Gln Met Met Thr Lys Glu Asp Gly
770 775 780

Lys His His Glu Val Asn Val Gln Phe Ser Trp Tyr Gly Thr Thr Ile
785 790 795 800

Lys Arg Asp Lys Ser Gly Ala Tyr Leu Phe Leu Pro Asp Gly Asn Ala
805 810 815

Lys Pro Tyr Val Tyr Thr Thr Pro Pro Phe Val Arg Val Thr His Gly
820 825 830

Arg Ile Tyr Ser Glu Val Thr Cys Phe Phe Asp His Val Thr His Arg
835 840 845

Val Arg Leu Tyr His Ile Gln Gly Ile Glu Gly Gln Ser Val Glu Val
850 855 860

Ser Asn Ile Val Asp Ile Arg Lys Val Tyr Asn Arg Glu Ile Ala Met
865 870 875 880

Lys Ile Ser Ser Asp Ile Lys Ser Gln Asn Arg Phe Tyr Thr Asp Leu
885 890 895

Asn Gly Tyr Gln Ile Gln Pro Arg Met Thr Leu Ser Lys Leu Pro Leu
900 905 910

Gln Ala Asn Val Tyr Pro Met Thr Thr Met Ala Tyr Ile Gln Asp Ala
915 920 925

Lys His Arg Leu Thr Leu Leu Ser Ala Gln Ser Leu Gly Val Ser Ser
930 935 940

Leu Asn Ser Gly Gln Ile Glu Val Ile Met Asp Arg Arg Leu Met Gln
945 950 955 960

Asp Asp Asn Arg Gly Leu Glu Gln Gly Ile Gln Asp Asn Lys Ile Thr
965 970 975

Ala Asn Leu Phe Arg Ile Leu Leu Glu Lys Arg Ser Ala Val Asn Thr
980 985 990

Glu Glu Glu Lys Lys Ser Val Ser Tyr Pro Ser Leu Leu Ser His Ile
995 1000 1005

Thr Ser Ser Leu Met Asn His Pro Val Ile Pro Met Ala Asn Lys
1010 1015 1020

Phe Phe Ser Pro Thr Leu Glu Leu Gln Gly Glu Phe Ser Pro Leu
1025 1030 1035

Gln Ser Ser Leu Pro Cys Asp Ile His Leu Val Asn Leu Arg Thr
1040 1045 1050

Ile Gln Ser Lys Val Gly Asn Gly His Ser Asn Glu Ala Ala Leu
1055 1060 1065

Ile Leu His Arg Lys Gly Phe Asp Cys Arg Phe Ser Ser Lys Gly
1070 1075 1080

Thr Gly Leu Phe Cys Ser Thr Thr Gln Gly Lys Ile Leu Val Gln
1085 1090 1095

Lys Leu Leu Asn Lys Phe Ile Val Glu Ser Leu Thr Pro Ser Ser
1100 1105 1110

Leu Ser Leu Met His Ser Pro Pro Gly Thr Gln Asn Ile Ser Glu
1115 1120 1125

Ile Asn Leu Ser Pro Met Glu Ile Ser Thr Phe Arg Ile Gln Leu
1130 1135 1140

Arg

<210> 19
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GalT

<400> 19
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
tcgctctacc tgatgctgga ccgggggtcac ttagactacc ccaggaaccc gcgccgcgag 120
ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180
ttgctagctg agaataatga gatcatctca aatattagag actcagtcac caatttgagt 240
gagtctgtgg aggatgggtcc gaaaagttca caaagcaatt tcagccaagg tgctgggtca 300
cccgcctgcc ctgaggagtc cccgctgctt gtgggccccca tgctgattga gtttaacatg 360
cctgtgggacc tggagctcgt ggcaaagcag aacccaaatg tgaagatggg cggccgctat 420
gccccaggg actgcgtctc tcctcacaag gtggccatca tcattccatt ccgcaaccgg 480
caggagcacc tcaagtactg gctatattat ttgcaccag tcctgcagcg ccagcagctg 540
gactatggca tctatgttat caaccaggcg ggagacacta tattcaatcg tgctaagctc 600
ctcaatgttg gctttcaaga agccttgaag gactatgact acacctgctt tgtgtttagt 660
gacgtggacc tcattccaat gaatgaccat aatgcgtaca ggtgtttttc acagccacgg 720
cacatttccg ttgcaatgga taagtttgga ttcagcctac cttatgttca gtattttgga 780
ggtgtctctg ctctaagtaa acaacagttt ctaaccatca atggatttcc taataattat 840
tggggctggg gaggagaaga tgatgacatt tttaacagat tagtttttag aggcattgtc 900
atatctcgcc caaatgctgt ggtcgggagg tgtcgcatga tccgccactc aagagacaaa 960

```
<210> 20
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GalT

<400> 20
```

Met 1	Lys	Leu	Ser	Arg 5	Gln	Phe	Thr	Val	Phe 10	Gly	Ser	Ala	Ile	Phe 15	Cys
Val	Val	Ile	Phe 20	Ser	Leu	Tyr	Leu	Met 25	Leu	Asp	Arg	Gly	His 30	Leu	Asp
Tyr	Pro	Arg 35	Asn	Pro	Arg	Arg	Glu 40	Gly	Ser	Phe	Pro	Gln 45	Gly	Gln	Leu
Ser	Met 50	Leu	Gln	Glu	Lys	Ile 55	Asp	His	Leu	Glu	Arg 60	Leu	Leu	Ala	Glu
Asn 65	Asn	Glu	Ile	Ile	Ser 70	Asn	Ile	Arg	Asp	Ser 75	Val	Ile	Asn	Leu	Ser 80
Glu	Ser	Val	Glu	Asp 85	Gly	Pro	Lys	Ser	Ser 90	Gln	Ser	Asn	Phe	Ser 95	Gln
Gly	Ala	Gly	Ser 100	Pro	Ala	Cys	Pro	Glu 105	Glu	Ser	Pro	Leu	Leu 110	Val	Gly
Pro	Met	Leu 115	Ile	Glu	Phe	Asn	Met 120	Pro	Val	Asp	Leu	Glu 125	Leu	Val	Ala
Lys	Gln 130	Asn	Pro	Asn	Val	Lys 135	Met	Gly	Gly	Arg	Tyr 140	Ala	Pro	Arg	Asp
Cys 145	Val	Ser	Pro	His	Lys 150	Val	Ala	Ile	Ile	Ile 155	Pro	Phe	Arg	Asn	Arg 160
Gln	Glu	His	Leu	Lys 165	Tyr	Trp	Leu	Tyr	Tyr 170	Leu	His	Pro	Val	Leu 175	Gln
Arg	Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	Asn	Gln	Ala	Gly	Asp

[illegible]